09786635 Results

SEQ ID NO: 1

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6880	100.0	6880	6	AX253450	AX253450 Sequence
2	6880	100.0	6880	9	HSA012376	AJ012376 Homo sapi
3	6880	100.0	7260	6	AX253452	AX253452 Sequence
4	6879	100.0	9497	6	AX059973	AX059973 Sequence
5	6879	100.0	9497	9	AF165281	AF165281 Homo sapi
6	6875.8	99.9	9741	6	AX127830	AX127830 Sequence
7	6875.8	99.9	9741	6	AX139817	AX139817 Sequence
8	6875.8	99.9	9741	6	AX351038	AX351038 Sequence
9	6875.8	99.9	9854	6	AX127831	AX127831 Sequence
10	6875.8	99.9	9854	6	AX139818	AX139818 Sequence
11	6870.4	99.9	7860	6	AX092594	AX092594 Sequence
12	6865	99.8	9495	6	AX059978	AX059978 Sequence
13	6862.4	99.7	10442	6	AX060713	AX060713 Sequence
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16	6860.8	99.7	10474	6	AX060719	AX060719 Sequence
17	6860.8	99.7	10474	6	AX060721	AX060721 Sequence
18	6860.8	99.7	10474	6	AX060898	AX060898 Sequence
19	6860.8	99.7	10474	6	AX060900	AX060900 Sequence
20	6845.2	99.5	7862	6	AX135712	AX135712 Sequence
21	6760.2	98.3	9593	6	AX059976	AX059976 Sequence
22	6711.6	97.6	6786	9	AB055982	AB055982 Homo sapi
23	5630	81.8	7878	10	MMABC1	X75926 Mus musculu
24	5455.6	79.3	6801	10	AY208182	AY208182 Rattus no
25	4302	62.5	7074	5	AF362377	AF362377 Gallus ga
26	2052.4	29.8	5097	6	BD012346	BD012346 Genes rel
27	2052.4	29.8	5097	6	BD160225	BD160225 Primer fo
28	2052.4	29.8	5097	9	AK027864	AK027864 Homo sapi
29	1911.6	27.8	7298	9	AF001945	AF001945 Homo sapi

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AF165281
LOCUS       AF165281              9497 bp    mRNA    linear   PRI 17-AUG-1999
DEFINITION  Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA,
            complete cds.
ACCESSION   AF165281
VERSION     AF165281.1  GI:5734100
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Tangier disease is caused by mutations in the gene encoding
            ATP-binding cassette transporter 1
  JOURNAL   Nat. Genet. 22 (4), 352-355 (1999)
  MEDLINE   99364413
   PUBMED   10431238
REFERENCE   2  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston
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BASE COUNT      2600 a    2115 c    2217 g    2564 t       1 others
ORIGIN

   Query Match            100.0%;   Score 6879;   DB 9;   Length 9497;
   Best Local Similarity   100.0%;   Pred. No. 0;
   Matches 6879;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Qy       61 TCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 120
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Qy      121 ATGCCCTCTGCAGGAACACTTCCTTGGGTTCAGGGGATTATCTGTAATGCCAACAACCCC 180
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Qy   2041 GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTC 2100
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Db   2041 GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTC 2100

Qy   2101 TTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC 2160
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Qy   2161 TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC 2220
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Qy   2461 TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCCCAGGCCCTGGTATTTTCCTTGC 2520
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Db   2461 TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCCCAGGCCCTGGTATTTTCCTTGC 2520

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Qy   2761 ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCCGACCTCGGGCACCGCCTACATCCTG 2820
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Db   2941 AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3000

Qy   3001 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGAATGCAGAGAAAG 3060
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Db   3001 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGAATGCAGAGAAAG 3060

Qy   3061 CTATCTGTGGCCTTGGCCTTTGTCGGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA 3120
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Db   3061 CTATCTGTGGCCTTGGCCTTTGTCGGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA 3120

Qy   3121 GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3180
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Db   3121 GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3180

Qy   3181 GGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG 3240
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Db   3181 GGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG 3240

Qy   3241 ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3300
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Qy   3301 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3360
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Db   3301 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3360

Qy   3361 TCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTTCTCAG 3420
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Qy      4621 CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT 4680
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Qy      4681 ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT 4740
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Qy      4741 GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAG 4800
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2	430.8	6.3	5894	3	US-08-762-500-24	Sequence 24, Appl
3	430.8	6.3	6525	3	US-08-762-500-74	Sequence 74, Appl
4	99.4	1.4	1008	4	US-09-252-991A-4266	Sequence 4266, Ap
c 5	98.8	1.4	999	4	US-09-252-991A-4588	Sequence 4588, Ap
6	89.4	1.3	1614	4	US-09-252-991A-4198	Sequence 4198, Ap
7	85.8	1.2	1824	4	US-09-252-991A-1780	Sequence 1780, Ap
8	83.8	1.2	1176	4	US-09-252-991A-3704	Sequence 3704, Ap
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10	81	1.2	36181	4	US-08-311-731A-120	Sequence 120, App
11	78.4	1.1	1548	4	US-09-252-991A-3653	Sequence 3653, Ap
c 12	77.4	1.1	762	4	US-09-252-991A-1938	Sequence 1938, Ap
c 13	76.6	1.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	75.2	1.1	969	4	US-09-107-532A-1008	Sequence 1008, Ap
15	75	1.1	1770	4	US-09-328-352-3466	Sequence 3466, Ap

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3600.4	52.3	4783	11	AK051920	AK051920 Mus muscu
2	1024.8	14.9	3605	11	AK052916	AK052916 Mus muscu
3	692.4	10.1	809	12	BI754756	BI754756 603025477
4	636.6	9.3	854	12	BI854140	BI854140 603381449
5	624.4	9.1	754	14	CD351847	CD351847 UI-M-GI0-
c 6	591.2	8.6	878	12	BI182779	BI182779 UNL-P-FN-
7	587.8	8.5	673	14	CD351490	CD351490 UI-M-GI0-
c 8	550.4	8.0	661	14	CB481810	CB481810 jns83_A02
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16	516	7.5	620	14	CA889361	CA889361 B0152D10-
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19	486.4	7.1	605	14	CB546553	CB546553 AMGNNUC:N
20	479.8	7.0	579	14	CA884367	CA884367 B0109G01-
21	477	6.9	1004	11	BC034824	BC034824 Homo sapi
22	473	6.9	562	10	BE665489	BE665489 154542 MA
23	459.4	6.7	515	10	BF094524	BF094524 MR0-UT004
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RESULT 1
AK051920
LOCUS       AK051920                4783 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
            enriched library, clone:D230019D04 product:ATP-binding cassette,
            sub-family A (ABC1), member 1, full insert sequence.
ACCESSION   AK051920
VERSION     AK051920.1  GI:26342297
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
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   ORGANISM  Mus musculus
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             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE   1
   AUTHORS   Carninci,P. and Hayashizaki,Y.
     TITLE   High-efficiency full-length cDNA cloning
   JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
    PUBMED   10349636
 REFERENCE   2
   AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
     TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
   JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
    PUBMED   11042159
 REFERENCE   3
   AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
     TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
   JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
    PUBMED   11076861
 REFERENCE   4
   AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
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             Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
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             Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
             Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
             Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
             Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
             Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
             Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
             Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
             Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
             and Hayashizaki,Y.
     TITLE   Functional annotation of a full-length mouse cDNA collection
   JOURNAL   Nature 409 (6821), 685-690 (2001)
   MEDLINE   21085660
    PUBMED   11217851
 REFERENCE   5
   AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
     TITLE   Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
   JOURNAL   Nature 420, 563-573 (2002)
 REFERENCE   6  (bases 1 to 4783)
   AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
             Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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             Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
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                    Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                    Muramatsu,M. and Hayashizaki,Y.
    TITLE   Direct Submission
    JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                    Physical and Chemical Research (RIKEN), Laboratory for Genome
                    Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                    RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                    Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                    URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                    Fax:81-45-503-9216)
    COMMENT   cDNA library was prepared and sequenced in Mouse Genome
                    Encyclopedia Project of Genome Exploration Research Group in Riken
                    Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                    Division of Experimental Animal Research in Riken contributed to
                    prepare mouse tissues.
                    Please visit our web site for further details.
                    URL:http://genome.gsc.riken.go.jp/
                    URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers
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ORIGIN

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    Matches 3901; Conservative   0; Mismatches 501; Indels   0; Gaps   0;

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Db   2362 CTCTGGTTTAGCTGGTTTGTTAGCAGCCTCATCCCTCTGCTTGTGAGCGCTGGCCTGCTG 2421

Qy   2041 GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTTGTC 2100
          ||||||||| |||||||||||||||||||||||||| ||||| |||||||||||||||| |||
Db   2422 GTGGTCATCTTGAAGTTAGGAAACCTGCTGCCCTATAGTGACCCCAGCGTGGTGTTCGTC 2481

Qy   2101 TTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC 2160
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Db   2482 TTCCTGTCTGTGTGTTTGCCATGGTGACCATCCTACAGTGCTTCCTCATTAGCACGCTCTTC 2541
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Qy   2161 TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC 2220
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Db   2542 TCCCGTGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC 2601

Qy   2221 TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC 2280
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Db   2602 TATGTGCTGTGCGTAGCCTGGCAGGACTATGTGGGCTTCTCCATCAAGATCTTTGCTAGC 2661

Qy   2281 CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAG 2340
          ||||||||||||||||||||||||  || ||||||||||| || ||||||| ||||||||
Db   2662 CTGCTGTCTCCTGTGGCTTTTGGATTCGGCTGTGAGTATTTCGCCCTTTTCGAGGAGCAA 2721

Qy   2341 GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT 2400
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Db   2722 GGTATCGGGGTCCAATGGGACAATCTCTTTGAGAGCCCGGTGGAGGAGGACGGCTTCAAT 2781

Qy   2401 CTCACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG 2460
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Db   2782 CTCACCACTGCAGTGTCCATGATGCTCTTTGACACCTTTCTCTATGGCGTGATGACATGG 2841

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Qy   2521 ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG 2580
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Db   2902 ACCAAGTCATACTGGTTTGGTGAGGAAATTGATGAGAAGAGCCACCCTGGTTCCAGCCAG 2961

Qy   2581 AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC 2640
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Db   3022 ATTCAGAACCTGGTGAAGGTTTACCGAGATGGCATGAAGGTTGCTGTGGATGGCTTGGCG 3081

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Qy   2761 ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCCGACCTCGGGCACCGCCTACATCCTG 2820
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Db   3142 ACCACCATGTCAATACTGACTGGGCTGTTTCCCCCAACTTCTGGCACGGCCTACATCCTG 3201

Qy   2821 GGAAAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG 2880
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Db   3202 GGGAAGGACATTCGCTCGGAGATGAGCTCCATCCGGCAGAACCTGGGAGTCTGTCCCCAG 3261

Qy   2881 CATAACGTGCTGTTTGACATGCTGACTGTCGAAGAACACATCTGGTTCTATGCCCGCTTG 2940
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Db   3262 CATAATGTGCTGTTTGACATGCTGACTGTCGAAGAGCACATCTGGTTCTATGCGCGCCTA 3321

Qy   2941 AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3000
          || |||||||| |||||||||||||| ||  || ||||||||||||||||||||||||||| |
Db   3322 AAGGGGCTCTCAGAGAAGCACGTGAAAGCAGAGATGGAGCAGATGGCCCTGGATGTTGGC 3381

Qy   3001 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGAATGCAGAGAAAG 3060
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Db   3382 TTACCCCCGAGCAAGCTGAAAAGCAAAACGAGTCAGCTCTCAGGTGGGATGCAGAGAAAG 3441

Qy   3061 CTATCTGTGGCCTTGGCCTTTGTCGGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA 3120
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Db   3442 CTGTCTGTGGCCTTGGCCTTCGTGGGGTGGATCCAAGGTTGTCATTCTGGACGAGCCCACA 3501

Qy   3121 GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3180
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Db   3502 GCCGGGGTGGACCCGTACTCTCGCAGGGGAATATGGGAACTCCTGCTAAAATACCGGCAA 3561

Qy   3181 GGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG 3240
          ||||||||||||||||||||||| | |||||||||||||||||| ||||| ||| |||| ||||||||
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Db   3562 GGCCGCACCATTATTTTGTCTACACACCACATGGACGAAGCTGACATCCTTGGGGACAGA 3621

Qy   3241 ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3300
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Qy   3301 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3360
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Qy   3361 TCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTTCTCAG 3420
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Qy   3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
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Qy   3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGGAAGACATA 3540
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Db   3862 TCTGCTATCTCCAACCTCATCAGGAAGCACGTGTCTGAAGCCCGGCTGGTGGAGGACATT 3921

Qy   3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
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Db   3922 GGGCACGAGCTGACCTATGTGCTGCCGTACGAAGCCGCGAAGGAGGGAGCCTTTGTGGAA 3981

Qy   3601 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3660
          |||||  |||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db   3982 CTCTTCCATGAGATTGATGACCGGCTCTCAGACCTGGGCATCTCCAGTTATGGCATCTCG 4041

Qy   3661 GAGACGACCCTGGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
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Db   4042 GAGACCACCCTGGAAGAAATATTCCTCAAAGTGGCTGAAGAGAGCGGGGTGGATGCTGAG 4101

Qy   3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
          ||||||||||||||| |||||||||||||||||||| |||||||||||||||||||||||||
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Qy   3781 TGTCTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA 3840
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Qy   3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCCTACCAGGTGAAA 3900
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Db   4222 GAATCCAGGGAGACCGACCTGCTCAGTGGGATGGACGGCAAAGGCTCCTACCAGCTGAAG 4281

Qy   3901 GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
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Db   4282 GGCTGGAAACTCACCCAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGGCTGCTGATTGCC 4341

Qy   3961 AGACGGAGTCGGAAAGGATTTTTTTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
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Db   4342 AGACGGAGCCGGAAGGGGTTTCTTTGCTCAGATTGTCCTGCCAGCTGTCTTTGTTTGCATT 4401

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Db   4402 GCCCTGGTCTTCAGCCTGATTGTGCCACCCTTTGGCAAGTACCCCAGCCTGGAACTTCAG 4461

Qy   4081 CCCTGGATGTACAACGAACAGTACACATTTGTCAGCAATGATGCTCCTGAGGACACGGGA 4140
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Db   4462 CCCTGGATGTATAATGAGCAGTATACATTTGTCAGTAATGATGCTCCCGAGGACATGGGC 4521

Qy   4141 ACCCTGGAACTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
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Db   4522 ACCCAGGAACTCCTGAATGCTCTGACCAAAGATCCAGGCTTTGGGACCCGCTGTATGGAA 4581

Qy   4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
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Db   4582 GGAAACCCAATCCCAGATACCCCCTTGCTTGGCTGGGGAGGAGGACTGGACCATCAGCCCC 4641

Qy   4261 GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCTTCA 4320
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Db  4642 GTCCCCCAGAGCATCGTGGACCTCTTCCAGAATGGAAACTGGACCATGAAGAACCCCTCA 4701

Qy  4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380
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Db  4702 CCTGCGTGCCAGTGTAGCAGTGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4761

Qy  4381 GCAGGGGGGCTGCCTCCTCCAC 4402
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SEQ ID NO: 2

Result No.	Score	Query Match	Length	DB	ID	Description
1	11469	100.0	2201	21	AAY79380	Human ATP binding
2	11469	100.0	2201	22	AAE13021	Human ATP binding
3	11469	100.0	2201	22	AAM50227	Human ATP binding
4	11469	100.0	2201	23	ABP65164	Hypoxia-regulated
5	11469	100.0	2261	22	AAE13022	Human ATP binding
6	11469	100.0	2261	22	AAM50228	Human ATP binding
7	11469	100.0	2261	22	AAU02176	Human ABC1. Homo
8	11469	100.0	2261	22	AAU02177	Human ABC1 mutant
9	11469	100.0	2261	23	ABB83111	Human ABCA1 transp
10	11469	100.0	2261	23	ABP52092	Homo sapiens ABC t
11	11469	100.0	2261	23	AAE23000	Human ABC1 full-le
12	11468	100.0	2261	23	ABB83117	Polymorphic human
13	11468	100.0	2261	23	ABB83124	Polymorphic human
14	11466	100.0	2261	22	AAU02183	Human ABC1 mutant
15	11466	100.0	2261	22	AAU02188	Human ABC1 mutant
16	11466	100.0	2261	23	ABB83115	Polymorphic human
17	11466	100.0	2261	23	ABB83116	Polymorphic human
18	11466	100.0	2261	23	ABB83119	Polymorphic human
19	11466	100.0	2261	23	ABB83122	Polymorphic human
20	11466	100.0	2261	23	ABB83123	Polymorphic human
21	11465	100.0	2261	22	AAU02189	Human ABC1 mutant
22	11464	100.0	2261	23	ABB83121	Polymorphic human
23	11463	99.9	2261	22	AAU02181	Human ABC1 mutant
24	11462	99.9	2261	22	AAM78550	Human protein SEQ
25	11462	99.9	2263	22	ABB11956	Human ABCA1 homolo
26	11462	99.9	2263	22	AAM79534	Human protein SEQ
27	11461	99.9	2261	22	AAU02182	Human ABC1 mutant
28	11461	99.9	2261	22	AAU02186	Human ABC1 mutant
29	11459	99.9	2261	23	ABB83118	Polymorphic human
30	11458	99.9	2261	23	ABB83120	Polymorphic human
31	11440	99.7	2261	21	AAB38082	Human ABC1 cholest
32	11440	99.7	2261	22	AAB71749	Human ABC1 protein
33	11440	99.7	2261	24	ABU11899	Human ATP-binding
34	11439	99.7	2261	23	ABB81578	Human ABC-A-1-1 pr
35	11437	99.7	2261	21	AAB38109	Human ABC1 cholest
36	11437	99.7	2261	21	AAB38111	Human ABC1 cholest
37	11437	99.7	2261	21	AAB38114	Human ABC1 cholest
38	11437	99.7	2261	21	AAB38115	Human ABC1 cholest
39	11437	99.7	2261	21	AAB38117	Human ABC1 cholest

No.	Score	Match	Length	DB	ID	Description
1	6909	60.2	1375	3	US-08-665-259-26	Sequence 26, Appl
2	6909	60.2	1375	3	US-08-762-500-26	Sequence 26, Appl
3	3129.5	27.3	1457	3	US-08-665-259-27	Sequence 27, Appl
4	3129.5	27.3	1457	3	US-08-762-500-27	Sequence 27, Appl
5	2635.5	23.0	1684	3	US-08-665-259-25	Sequence 25, Appl
6	2635.5	23.0	1684	3	US-08-762-500-25	Sequence 25, Appl
7	2635.5	23.0	1704	3	US-08-762-500-75	Sequence 75, Appl

8	359	3.1	315	4	US-09-328-352-4388	Sequence 4388, Ap
9	354	3.1	332	4	US-09-107-532A-3752	Sequence 3752, Ap
10	352.5	3.1	335	4	US-09-252-991A-20837	Sequence 20837, A
11	352	3.1	322	4	US-09-107-532A-4662	Sequence 4662, Ap
12	346	3.0	589	4	US-09-328-352-7592	Sequence 7592, Ap
13	336.5	2.9	1280	2	US-08-583-276-19	Sequence 19, Appl
14	335.5	2.9	291	4	US-09-107-532A-4205	Sequence 4205, Ap
15	335.5	2.9	1280	4	US-09-767-594-2	Sequence 2, Appli
16	335.5	2.9	1280	6	5206352-4	Patent No. 5206352
17	333	2.9	1279	2	US-08-784-649A-2	Sequence 2, Appli
18	332	2.9	402	4	US-09-107-532A-5360	Sequence 5360, Ap
19	330.5	2.9	1280	2	US-08-752-447-2	Sequence 2, Appli

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RESULT 1
US-08-665-259-26
; Sequence 26, Application US/08665259
; Patent No. 6028173
;   GENERAL INFORMATION:
;     APPLICANT:  Landes, Gregory M.
;     APPLICANT:  Burn, Timothy C.
;     APPLICANT:  Connors, Timothy D.
;     APPLICANT:  Dackowski, William R.
;     APPLICANT:  Van Raay, Terence J.
;     APPLICANT:  Klinger, Katherine W.
;     TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
;     TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
;     NUMBER OF SEQUENCES:  73
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  GENZYME CORPORATION
;       STREET:  One Mountain Road
;       CITY:  Framingham
;       STATE:  Massachusetts
;       COUNTRY:  United States of America
;       ZIP:  01701
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/665,259
;       FILING DATE:  17-JUN-1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Dugan, Deborah A.
;       REGISTRATION NUMBER:  37,315
;       REFERENCE/DOCKET NUMBER:  IG5-9.1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (508) 872-8400
;       TELEFAX:  (508) 872-5415
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1375 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
US-08-665-259-26

  Query Match            60.2%;  Score 6909;  DB 3;  Length 1375;
  Best Local Similarity  96.9%;  Pred. No. 0;
  Matches 1332;  Conservative  21;  Mismatches  22;  Indels  0;  Gaps  0;

Qy      827 CMEEEPTHLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 886
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Db        1 CMEEEPTHLRLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 60

Qy      887 TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEK 946
                     ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
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Db       61 TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEK 120

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            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      121 HVKAEMEQMALDVGLPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 180

Qy     1007 SRRGIWELLLKYRQGRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGY 1066
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Db      181 SRRGIWELLLKYRQGRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSLFLKNQLGTGY 240

Qy     1067 YLTLVKKDVESSLSSCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNL 1126
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Qy     1127 IRKHVSEARLVEDIGHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEE 1186
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Db      301 IRKHVSEARLVEDIGHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEE 360

Qy     1187 IFLKVAEESGVDAETSDGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETD 1246
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Db      361 IFLKVAEESGVDAETSDGTLPARRNRRAFGDKQSCLHPFTEDDAVDPNDSDIDPESRETD 420

Qy     1247 LLSGMDGKGSYQVKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 1306
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Db      421 LLSGMDGKGSYQLKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 480

Qy     1307 IVPPFGKYPSLELQPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPD 1366
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Qy     1367 TPCQAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP 1426
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Qy     1427 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 1486
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Db      601 PQRKQKTADILQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALP 660

Qy     1487 PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 1546
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Db      661 PSHEVNDAIKQMKKLLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFL 720

Qy     1547 NVINNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMS 1606
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Db      721 NVINNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMS 780

Qy     1607 FVPASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQ 1666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 FVPASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQ 840

Qy     1667 KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 1726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 900

Qy     1727 VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 1786
            ||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 VLELFTNNKLNDINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 960

Qy     1787 DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1846
            ||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Db      961 DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVKAKLPPLNDEDEDVRRERQRILDGG 1020

Qy     1847 GQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVT 1906
            ||||||||||||||||||||||||||:|||||||||||||||||||:|||||||||| ||
Db     1021 GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGDTPVT 1080

Qy     1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGE 1966
            |||||||:||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     1081 RGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGE 1140

Qy     1967 WAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 2026
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                 |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    1141  WAIRKLGLVKYGEKYASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 1200

Qy    2027  ALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 2086
                 |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  ALSIVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 1260

Qy    2087  GSNPDLKPVQDFFGLAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 2146
                 |||||||||||:||||||||||| |||||||||||||||||||||||||||||||||
Db    1261  GSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 1320

Qy    2147  SVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  SVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 1375
```

RESULT 2
US-08-762-500-26
; Sequence 26, Application US/08762500
; Patent No. 6030806
;   GENERAL INFORMATION:
;   APPLICANT: Landes, Gregory M.
;   APPLICANT: Burn, Timothy C.
;   APPLICANT: Connors, Timothy D.
;   APPLICANT: Dackowski, William R.
;   APPLICANT: Van Raay, Terence J.
;   APPLICANT: Klinger, Katherine W.
;   TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
;   TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
;   NUMBER OF SEQUENCES: 83
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: GENZYME CORPORATION
;   STREET: One Mountain Road
;   CITY: Framingham
;   STATE: Massachusetts
;   COUNTRY: United States of America
;   ZIP: 01701
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/762,500
;   FILING DATE: 09-DEC-1996
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/665,259
;   FILING DATE: 17-JUN-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US96/10469
;   FILING DATE: 17-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Dugan, Deborah A.
;   REGISTRATION NUMBER: 37,315
;   REFERENCE/DOCKET NUMBER: IG5-9.3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (508) 872-8400
;   TELEFAX: (508) 872-5415
;   INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1375 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: unknown
;   MOLECULE TYPE: protein
US-08-762-500-26

    Query Match   60.2%; Score 6909; DB 3; Length 1375;

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Best Local Similarity    96.9%;  Pred. No. 0;
Matches 1332;  Conservative    21;  Mismatches    22;  Indels     0;  Gaps    0;

Qy       827  CMEEEPTHLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL  886
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db         1  CMEEEPTHLRLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL  60

Qy       887  TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEK  946
              ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        61  TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEK  120

Qy       947  HVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY  1006
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       121  HVKAEMEQMALDVGLPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY  180

Qy      1007  SRRGIWELLLKYRQGRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGY  1066
              |||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db       181  SRRGIWELLLKYRQGRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSLFLKNQLGTGY  240

Qy      1067  YLTLVKKDVESSLSSCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNL  1126
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       241  YLTLVKKDVESSLSSCRNSSSTVSCLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNL  300

Qy      1127  IRKHVSEARLVEDIGHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEE  1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301  IRKHVSEARLVEDIGHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEE  360

Qy      1187  IFLKVAEESGVDAETSDGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETD  1246
              |||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db       361  IFLKVAEESGVDAETSDGTLPARRNRRAFGDKQSCLHPFTEDDAVDPNDSDIDPESRETD  420

Qy      1247  LLSGMDGKGSYQVKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL  1306
              |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db       421  LLSGMDGKGSYQLKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL  480

Qy      1307  IVPPFGKYPSLELQPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPD  1366
              |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db       481  IVPPFGKYPSLELQPWMYNEQYTFVSNDAPEDMGTQELLNALTKDPGFGTRCMEGNPIPD  540

Qy      1367  TPCQAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP  1426
              ||| ||||:|| :||||:|:|||||||||||:||||||||||||||||||||||||||||
Db       541  TPCLAGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP  600

Qy      1427  PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP  1486
              ||||| ||||||:||||||||||||||||||||||||||||||||||||||||||:||||
Db       601  PQRKQKTADILQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALP  660

Qy      1487  PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL  1546
              || ||||| ||||| ||| ||:|||||:||||| |||:|||||||||||||||||||||
Db       661  PSHEVNDAIKQMKKLLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFL  720

Qy      1547  NVINNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMS  1606
              |||||||||||||||||||| ||||||||||||||||||||| |||||||||||||||||
Db       721  NVINNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMS  780

Qy      1607  FVPASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQ  1666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781  FVPASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQ  840

Qy      1667  KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF  1726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841  KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF  900

Qy      1727  VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW  1786
              ||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db       901  VLELFTNNKLNDINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW  960

Qy      1787  DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG  1846
              |||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Db       961  DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVKAKLPPLNDEDEDVRRERQRILDGG  1020
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Qy   1847  GQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVT 1906
            |||||||||||||||||||||||||||||:|||||||||||||||||||||:|||||||| ||
Db   1021  GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGDTPVT 1080


Qy   1907  RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGE 1966
            |||||||:||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1081  RGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGE 1140


Qy   1967  WAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 2026
            |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1141  WAIRKLGLVKYGEKYASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 1200


Qy   2027  ALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 2086
            |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  ALSIVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 1260


Qy   2087  GSNPDLKPVQDFFGLAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 2146
            |||||||||:|||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1261  GSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 1320


Qy   2147  SVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  SVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 1375
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10906	95.1	2201	2	A54774	ATP binding casset
2	3338.5	29.1	1529	2	A59189	ATP-binding casset
3	3129.5	27.3	1472	2	B54774	ATP binding casset
4	2638.5	23.0	1704	2	S71363	probable ATP-bindi
5	2635.5	23.0	1704	2	A59188	ATP-binding casset
6	2061	18.0	1802	2	T33783	hypothetical prote
7	1975	17.2	1816	2	A84845	probable ABC trans
8	1854.5	16.2	1447	2	T15200	hypothetical prote
9	1792	15.6	1317	2	C88925	protein F33E11.4 [
10	1535.5	13.4	1758	2	F88559	protein C48B4.4b [
11	1528.5	13.3	1704	2	T42749	ATP-binding casset
12	1526	13.3	1767	2	S60124	transport protein
13	1393	12.1	1246	2	T00826	hypothetical prote
14	1150.5	10.0	1564	2	T27121	hypothetical prote
15	1006.5	8.8	373	2	T47150	hypothetical prote
16	1005.5	8.8	1431	2	T22748	hypothetical prote
17	846	7.4	269	2	T46467	hypothetical prote
18	786.5	6.9	1011	2	T07712	probable ABC-type
19	695	6.1	900	2	T07717	probable ABC-type

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RESULT 1
A54774
ATP binding cassette transporter ABC1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001
C;Accession: A54774
R;Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.
Genomics 21, 150-159, 1994
A;Title: Cloning of two novel ABC transporters mapping on human chromosome 9.
A;Reference number: A54774; MUID:94375008; PMID:8088782
A;Accession: A54774
A;Molecule type: mRNA
A;Residues: 1-2201 <LUC>
A;Cross-references: GB:X75926; NID:g495256; PIDN:CAA53530.1; PID:g495257
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; duplication; nucleotide binding; P-loop
F;856-1047/Domain: ATP-binding cassette homology <ABC1>
F;873-880/Region: nucleotide-binding motif A (P-loop)
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F;1869-2060/Domain: ATP-binding cassette homology <ABC2>
F;1886-1893/Region: nucleotide-binding motif A (P-loop)

```
    Query Match          95.1%;  Score 10906;  DB 2;  Length 2201;
    Best Local Similarity  94.8%;  Pred. No. 0;
    Matches 2087;  Conservative  54;  Mismatches  60;  Indels  0;  Gaps  0;
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```
Qy       1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT 60
           ||||||||||||||||||||||||||||||||||||||||||:||||||:|||||||:|||
Db       1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVSRLFSDAQRLLLYSQRDT 60

Qy      61 SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH 120
           |:||| |||| |:||| :|||||||||||||||||| ||||||:|||| :|::|| | |
Db      61 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSLPRSTVDSLLQXNVGLQ 120

Qy     121 KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLPREKLAAAERVLRSNMDILKPIL 180
           |||||||||| |||||||| ||:|||| ||| |||||:|| |||||||| |||||||::
Db     121 KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAAERVLRYNMDILKPVV 180

Qy     181 RTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMRSWSDMRQEVMFLTNVNSSSSSTQI 240
           ||||| |:: |||| || ||| |||||||| :|||||||||||||||||||||||||||
Db     181 TKLNSTSHLPTQHLAEATTVLLDSLGGLAQELFSTKSWSDMRQEVMFLTNVNSSSSSTQI 240

Qy     241 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK 300
           ||||||||||||||||||||||||||||||||||||| |||| :|||||||||||||||||
Db     241 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNNTEEDVDTFYDNSTTPYCNDLMK 300

Qy     301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 360

Qy     361 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAQDIVAFLAKHPEDVQSSNGS 420
           |:||||||||||||||||:||||| |||| :|||||||||||||:||||:|||||||:|||
Db     361 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTAQDIMAFLAKNPEDVQSPNGS 420

Qy     421 VYTWREAFNETNQAIRTISRFMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIVFTG 480
           |||||||||||||||:|||||||||||||||||| |||:||||||||||||||||||||||
Db     421 VYTWREAFNETNQAIQTISRFMECVNLNKLEPIPTEVRLINKSMELLDERKFWAGIVFTG 480

Qy     481 ITPGSIELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540
           ||| |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ITPDSVELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540

Qy     541 EQAIIRVLTGTEKKTGVYMQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIV 600
           |||||||||:|||||||:|||||||||||||||||||||||||||||||||||||||||:||
Db     541 EQAIIRVLTGSEKKTGVYVQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKSIV 600

Qy     601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 660
           ||||||||||||||||||| |||||||:||||||||||||||||||||||||||||||||||
Db     601 YEKEARLKETMRIMGLDNGILWFSWFVSSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 660

Qy     661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
           ||||||:|||||||||||||||||||||||||||||||||||||||||||||||:|:|||||
Db     661 FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFAS 720

Qy     721 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTW 780
           ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db     721 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTAVSMMLFDTFLYGVMTW 780

Qy     781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVS 840
           |||||||||||||||||||||||||||||| ||||||||:|| :||||||||||||:||||
Db     781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPTHLRLGVS 840

Qy     841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNAGKTTTMSILTGLFPPTSGTAYIL 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNAGKTTTMSILTGLFPPTSGTAYIL 900

Qy     901 GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVG 960
           |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVG 960
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Qy    961 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLLKYRQ 1020
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 LPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLLKYRQ 1020

Qy   1021 GRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLS 1080
           ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLS 1080

Qy   1081 SCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 SCRNSSSTVSCLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140

Qy   1141 GHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200

Qy   1201 TSDGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK 1260
           |||||||||||||||||||||| ||||||| :|||||||||||||||||||||||||:|
Db   1201 TSDGTLPARRNRRAFGDKQSCLHPFTEDDAVDPNDSDIDPESRETDLLSGMDGKGSYQLK 1260

Qy   1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1320

Qy   1321 PWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEWTTAP 1380
           |||||||||||||||||| || ||||||||||||||||||||||||| |||| :|| :|
Db   1321 PWMYNEQYTFVSNDAPEDMGTQELLNALTKDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1380

Qy   1381 VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL 1440
           |||:|:|||||||||:|||||||||||||||||||||||||||||||||| ||||||:|
Db   1381 VPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQKTADILQNL 1440

Qy   1441 TGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500
           |||||||||||||||||||||||||||||||||||||||||:||||||| |||||| ||||
Db   1441 TGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1500

Qy   1501 HLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1560
           ||| ||:||||||:|||||| ||||:|||||||||||||||||||||||||||||||||
Db   1501 LLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1560

Qy   1561 GENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVVFLIQER 1620
           ||||| |||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   1561 GENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVVFLIQER 1620

Qy   1621 VSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 VSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL 1680

Qy   1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||:||||:||
Db   1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN 1740

Qy   1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800

Qy   1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
           |||||||||||||||||||||| ||| |||||||||||||||||||||||||||||||||
Db   1801 VVFFLITVLIQYRFFIRPRPVKAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860

Qy   1861 YRRRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVTRGDAFLNRNSILSN 1920
           |||||||||||||:|||||||||||||||||:|||||||||||:||||||||:||||||
Db   1861 YRRRKPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGDTPVTRGDAFLNKNSILSN 1920

Qy   1921 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGEWAIRKLGLVKYGEK 1980
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1921 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIRKLGLVKYGEK 1980

Qy   1981 YAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT 2040
           || ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   1981 YASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT 2040
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Qy   2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG 2100

Qy   2101 LAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF 2160
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF 2160

Qy   2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
          ||||||||||||||||||||||||||||||||||||||||
Db   2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	11466	100.0	2261	1	ABC1_HUMAN	O95477	homo sapien
2	10906	95.1	2261	1	ABC1_MOUSE	P41233	mus musculu
3	5689.5	49.6	2273	1	ABCR_HUMAN	P78363	homo sapien
4	4131	36.0	2436	1	ABC2_HUMAN	Q9bzc7	homo sapien
5	3989.5	34.8	2434	1	ABC2_MOUSE	P41234	mus musculu
6	2635.5	23.0	1704	1	ABC3_HUMAN	Q99758	homo sapien
7	1528.5	13.3	1704	1	CED7_CAEEL	P34358	caenorhabdi
8	411	3.6	330	1	DRRA_STRPE	P32010	streptomyce
9	380.5	3.3	343	1	NODI_RHISN	P55476	rhizobium s
10	366	3.2	304	1	NODI_RHIS3	P72335	rhizobium s
11	347	3.0	308	1	YADG_ECOLI	P36879	escherichia
12	347	3.0	335	1	NDI2_RHIME	Q8gnh6	rhizobium m
13	344.5	3.0	340	1	NODI_RHILO	P23703	rhizobium l
14	343.5	3.0	347	1	NODI_RHIGA	P50332	rhizobium g
15	335.5	2.9	1280	1	MDR1_HUMAN	P08183	homo sapien
16	331.5	2.9	355	1	NDI1_RHIME	O52618	rhizobium m
17	329.5	2.9	578	1	YBHF_ECOLI	P75776	escherichia
18	327	2.9	894	1	YHIH_ECOLI	P37624	escherichia
19	327	2.9	1276	1	MDR3_MOUSE	P21447	mus musculu

```
RESULT 2
ABC1_MOUSE
ID   ABC1_MOUSE      STANDARD;      PRT;   2261 AA.
AC   P41233;
DT   01-FEB-1995 (Rel. 31, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE   transporter 1) (ATP-binding cassette 1) (ABC-1).
GN   ABCA1 OR ABC1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2; TISSUE=Macrophage;
RX   MEDLINE=94375008; PubMed=8088782;
RA   Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT   "Cloning of two novel ABC transporters mapping on human chromosome
RT   9.";
RL   Genomics 21:150-159(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21251004; PubMed=11352567;
RA   Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT   "Human and mouse ABCA1 comparative sequencing and transgenesis
```

RT   studies revealing novel regulatory sequences.";
RL   Genomics 73:66-76(2001).
CC   -!- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
CC   TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
CC   TRANSPORT (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC   LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC   -!- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC   EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC   ATP BINDING CASSETTE (ABC) DOMAIN.
CC   -!- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By
CC   similarity).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   --
DR   EMBL; X75926; CAA53530.1; ALT_INIT.
DR   EMBL; AF287263; AAG39073.1; ALT_INIT.
DR   MGD; MGI:99607; Abca1.
DR   GO; GO:0008203; P:cholesterol metabolism; IDA.
DR   GO; GO:0030301; P:cholesterol transport; IDA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.
FT   TRANSMEM   26   42   POTENTIAL.
FT   TRANSMEM   640   656   POTENTIAL.
FT   TRANSMEM   690   706   POTENTIAL.
FT   TRANSMEM   717   733   POTENTIAL.
FT   TRANSMEM   749   765   POTENTIAL.
FT   TRANSMEM   771   787   POTENTIAL.
FT   TRANSMEM   1041   1057   POTENTIAL.
FT   TRANSMEM   1351   1367   POTENTIAL.
FT   TRANSMEM   1661   1677   POTENTIAL.
FT   TRANSMEM   1708   1724   POTENTIAL.
FT   TRANSMEM   1737   1753   POTENTIAL.
FT   TRANSMEM   1775   1791   POTENTIAL.
FT   TRANSMEM   1854   1870   POTENTIAL.
FT   NP_BIND   933   940   ATP (POTENTIAL).
FT   NP_BIND   1946   1953   ATP (POTENTIAL).
FT   MOD_RES   1042   1042   PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT   SIMILARITY).
FT   MOD_RES   2054   2054   PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT   SIMILARITY).
FT   CARBOHYD   14   14   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   98   98   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151   151   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   161   161   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   196   196   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   244   244   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   292   292   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   337   337   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   349   349   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   400   400   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   478   478   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   489   489   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   521   521   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   820   820   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 1144   1144   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 1294   1294   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 1453   1453   N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT   CARBOHYD     1499     1499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     1504     1504       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     1637     1637       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     2044     2044       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     2238     2238       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     1567     1568       MISSING (IN REF. 2).
FT   CONFLICT     2024     2024       MISSING (IN REF. 2).
SQ   SEQUENCE     2261 AA;  254011 MW;  FAE62B21FD1D09F9 CRC64;

     Query Match          95.1%;  Score 10906;  DB 1;  Length 2261;
     Best Local Similarity  94.8%;  Pred. No. 0;
     Matches 2087;  Conservative   54;  Mismatches   60;  Indels    0;  Gaps    0;

Qy        1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT 60
            |||||||||||||||||||||||||||||||||||||||||||:|||||||:||||||||:||
Db       61 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVSRLFSDAQRLLLYSQRDT 120

Qy       61 SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH 120
            |:|||  |||| |:|||   :||||||||||||||||| ||||||:|||| :|:  :| |
Db      121 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSLPRSTVDSLLQXNVGLQ 180

Qy      121 KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLPREKLAAAERVLRSNMDILKPIL 180
            |||||||||||| ||||||| ||:|||| ||| ||||||:|| |||||||:|| ||||||| ||||||::
Db      181 KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAAERVLRYNMDILKPVV 240

Qy      181 RTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMRSWSDMRQEVMFLTNVNSSSSSTQI 240
              ||||| |:: ||||| || ||| ||||||| :|||||||||||||||||||||||||||
Db      241 TKLNSTSHLPTQHLAEATTVLLDSLGGLAQELFSTKSWSDMRQEVMFLTNVNSSSSSTQI 300

Qy      241 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK 300
            |||||||||||||||||||||||||||||||||||||| |||| :||||||||||||||||
Db      301 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNNTEEDVDTFYDNSTTPYCNDLMK 360

Qy      301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 420

Qy      361 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAQDIVAFLAKHPEDVQSSNGS 420
            |:|||||||||||||||||||| ||||| || ||||:||||||||||||:|||||:|||||| |||
Db      421 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTAQDIMAFLAKNPEDVQSPNGS 480

Qy      421 VYTWREAFNETNQAIRTISRFMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIVFTG 480
            ||||||||||||||:|||||||||||||||||||||| ||| ||||||||||||||||||
Db      481 VYTWREAFNETNQAIQTISRFMECVNLNKLEPIPTEVRLINKSMELLDERKFWAGIVFTG 540

Qy      481 ITPGSIELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540
            ||| |:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ITPDSVELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 600

Qy      541 EQAIIRVLTGTEKKTGVYMQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIV 600
            |||||||||:|||||||:||||||||||||||||||||||||||||||||||||||| ||
Db      601 EQAIIRVLTGSEKKTGVYVQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKSIV 660

Qy      601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 660
            ||||||||||||||||||| |||||||:||||||||||||||||||||||||||||||||
Db      661 YEKEARLKETMRIMGLDNGILWFSWFVSSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 720

Qy      661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
            ||||||:|||||||||||||||||||||||||||||||||||||||||||||||::||||
Db      721 FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFAS 780

Qy      721 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTW 780
            ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db      781 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTAVSMMLFDTFLYGVMTW 840

Qy      781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVS 840
            |||||||||||||||||||||||||||||||| |||||||||:|| :|||||||||||:||||
Db      841 YIEAVFPGQYGIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPTHLRLGVS 900

Qy      841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      901  IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 960

Qy      901  GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVG 960
             ||||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  GKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVG 1020

Qy      961  LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1020
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  LPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1080

Qy     1021  GRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLS 1080
             ||||||||||||||| :|||||||||||||||||||||||||||||||||||||||||||
Db     1081  GRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLS 1140

Qy     1081  SCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  SCRNSSSTVSCLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1200

Qy     1141  GHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  GHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1260

Qy     1201  TSDGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK 1260
             ||||||||||||||||||||||| |||||||| |||||||||||||||||||||||||:|
Db     1261  TSDGTLPARRNRRAFGDKQSCLHPFTEDDAVDPNDSDIDPESRETDLLSGMDGKGSYQLK 1320

Qy     1261  GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1380

Qy     1321  PWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEWTTAP 1380
             ||||||||||||||||||| || |||||||||||||||||||||||||| ||||:|| :|
Db     1381  PWMYNEQYTFVSNDAPEDMGTQELLNALTKDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1440

Qy     1381  VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL 1440
             |||:|:||||||||||:||||||||||||||||||||||||||||||||||| ||||||:|
Db     1441  VPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQKTADILQNL 1500

Qy     1441  TGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500
             |||||||||||||||||||||||||||||||||||||||||:||||| ||||| |||||
Db     1501  TGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1560

Qy     1501  HLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1560
             ||| ||:||||||:||||| ||||:||||||||||||||||||||||||||||||||||
Db     1561  LLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1620

Qy     1561  GENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVVFLIQER 1620
             ||||| ||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     1621  GENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVVFLIQER 1680

Qy     1621  VSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681  VSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL 1740

Qy     1681  LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||:||||:||
Db     1741  LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN 1800

Qy     1741  DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801  DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1860

Qy     1801  VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
             |||||||||||||||||||||| ||| |||||||||||||||||||||||||||||||||
Db     1861  VVFFLITVLIQYRFFIRPRPVKAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1920

Qy     1861  YRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVTRGDAFLNRNSILSN 1920
             |||||||||||||:||||||||||||||||||||||||||||||:|||||||||||:||||||
Db     1921  YRRKRKPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGDTPVTRGDAFLNKNSILSN 1980

Qy     1921  IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGEWAIRKLGLVKYGEK 1980
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Db    1981  IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIRKLGLVKYGEK  2040

Qy    1981  YAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT  2040
             ||  |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db    2041  YASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT  2100

Qy    2041  SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG  2100
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db    2101  SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG  2160

Qy    2101  LAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF  2160
             |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF  2220

Qy    2161  AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV  2201
             |||||||||||||||||||||||||||||||||||||||||
Db    2221  AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV  2261
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